

**IN THE SPECIFICATION**

Please enter the substitute Sequence Listing into the specification in accordance with 37 C.F.R. § 1.825.

Please amend the specification as follows:

On page 4, amend the third full paragraph as follows:

In WO 98/39031, Rice et al. disclosed authentic HCV genome RNA sequences, in particular containing: a) the highly conserved 5'-terminal sequence "GCCAGCC" (SEQ ID NO. 26); b) the HCV polyprotein coding region; and c) 3'-NTR authentic sequences.

On page 4, amend the fourth full paragraph as follows:

In WO 99/04008, Purcell et al. disclosed an HCV infectious clone that also contained only the highly conserved 5'-terminal sequence "GCCAGC" (SEQ ID NO. 27).

On page 7, under DETAILED DESCRIPTION OF THE DRAWINGS amend the first paragraph as follows:

Figure 1 is a schematic view of the bi-cistronic replicon RNA. The sequence deviations between the I377/NS2-3' replicon from Lohman et al., 1999 Science 285: 110-113 and the APGK12 replicon are indicated below the replicon. In place of a G nucleotide at the +1 position in the I377/NS2-3' replicon, the APGK12 contains an additional G resulting in GG at the 5' terminus (the first G being counted as position -1). In the linker region between the neo gene and the EMCV IRES sequence two areas deviate from I377/NS2-3': 14 nucleotides (CGCGCCCAGATGTT) (SEQ ID NO. 28) which are not present in I377/NS2/3 are inserted at position 1184 in APGK12; 11 nucleotides (1231-1241) present in I377/NS2-3' are deleted to

generate APGK-12. In the NS5B coding region, a T at position 8032 was mutated to C to eliminate a NcoI restriction site.